SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Goodearl, Andrew
                                        Stroobant, Paul
                                        Minghetti, Luisa
                                        Waterfield, Michael
                                        Marchionni, Mark
                                        Chen, Mario
                                        Hiles, Ian

    (ii) TITLE OF INVENTION: GLIAL MITOGENIC FACTORS, THEIR
                                        PREPARATION AND USE

    (iii) NUMBER OF SEQUENCES: 189

    (iv) CORRESPONDENCE ADDRESS:

        (A) ADDRESSEE: Clark & Elbing LLP
        (B) STREET: 176 Federal Street
        (C) CITY: Boston
        (D) STATE: Massachusetts
        (E) COUNTRY: U.S.A.
        (F) ZIP: 02110

    (v) COMPUTER READABLE FORM:

        (A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
        (B) COMPUTER: IBM Compatible Pentium
        (C) OPERATING SYSTEM: Windows95
        (D) SOFTWARE: FastSeq Version 2.0

    (vi) CURRENT APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/736,019
        (B) FILING DATE: 22-OCT-1996
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/471,833
        (B) FILING DATE: 06-JUN-1995

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 08/036,555
        (B) FILING DATE: 24-MAR-1993

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 07/965,173
        (B) FILING DATE: 23-OCT-1992

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 07/907,138
        (B) FILING DATE: 30-JUN-1992

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: 07/940,389
        (B) FILING DATE: 03-SEP-1992

    (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/863,703
        (B) FILING DATE: 03-APR-1992

    (vii) PRIOR APPLICATION DATA:

        (A) APPLICATION NUMBER: UK 91 07566.3
        (B) FILING DATE: 10-APR-1991

    (viii) ATTORNEY/AGENT INFORMATION:

        (A) NAME: Bieker-Brady, Kristina
        (B) REGISTRATION NUMBER: 39,109
        (C) REFERENCE/DOCKET NUMBER: 04585/00200Q

    (ix) TELECOMMUNICATION INFORMATION:

        (A) TELEPHONE: (617) 428-0200
        (B) TELEFAX: (617) 428-7045
        (C) TELEX:

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Lys Gly Asp Ala His Thr Glu
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys

  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:

(D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 10 is unknown.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 9
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 7
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 16
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine and Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 8 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg

1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 7 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:

    (i) SEQUENCE CHARACTERISTICS:

```
        (A)  LENGTH:              11
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine.


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala

  1                 5                    10


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    14:

    (i) SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              10
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys

  1                 5                    10


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    15:

    (i) SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              8
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
  1                 5


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    16:

    (i) SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              6
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear
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    (ix) FEATURE:

        (D)  OTHER INFORMATION:  Xaa in position 1 is Lysine or Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
 1               5


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    17:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:            16
        (B) TYPE:              amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY:          linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:


Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1               5                  10                  15


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    18:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:            10
        (B) TYPE:              amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY:          linear

    (ix) FEATURE:

        (D)  OTHER INFORMATION:  Xaa in position 8 is unknown.


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
 1               5                  10


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    19:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:            7
        (B) TYPE:              amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY:          linear

    (ix) FEATURE:

        (D)  OTHER INFORMATION:  Xaa in position 2 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
 1               5
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 26
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

```
Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
 1               5                  10                  15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
              20                  25
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 2003
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in positions 31 and 32 could be
either A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

```
GGAATTCCTT TTTTTTTTTT TTTTTTTCTT NNTTTTTTTT TGCCCTTATA CCTCTTCGCC    60

TTTCTGTGGT TCCATCCACT TCTTCCCCCT CCTCCTCCCA TAAACAACTC TCCTACCCCT   120

GCACCCCCAA TAAATAAATA AAAGGAGGAG GGCAAGGGGG GAGGAGGAGG AGTGGTGCTG   180

CGAGGGGAAG GAAAAGGGAG GCAGCGCGAG AAGAGCCGGG CAGAGTCCGA ACCGACAGCC   240

AGAAGCCCGC ACGCACCTCG CACC ATG AGA TGG CGA CGC GCC CCG CGC CGC     291
                           Met Arg Trp Arg Arg Ala Pro Arg Arg
                            1               5

TCC GGG CGT CCC GGC CCC CGG GCC CAG CGC CCC GGC TCC GCC GCC CGC    339
Ser Gly Arg Pro Gly Pro Arg Ala Gln Arg Pro Gly Ser Ala Ala Arg
 10              15                  20                  25

TCG TCG CCG CCG CTG CCG CTG CTG CCA CTA CTG CTG CTG CTG GGG ACC    387
Ser Ser Pro Pro Leu Pro Leu Leu Pro Leu Leu Leu Leu Leu Gly Thr
             30                  35                  40

GCG GCC CTG GCG CCG GGG GCG GCG GCC GGC AAC GAG GCG GCT CCC GCG    435
Ala Ala Leu Ala Pro Gly Ala Ala Ala Gly Asn Glu Ala Ala Pro Ala
             45                  50                  55

GGG GCC TCG GTG TGC TAC TCG TCC CCG CCC AGC GTG GGA TCG GTG CAG    483
Gly Ala Ser Val Cys Tyr Ser Ser Pro Pro Ser Val Gly Ser Val Gln
         60                  65                  70

GAG CTA GCT CAG CGC GCC GCG GTG GTC ATC GAG GGA AAG GTG CAC CCG    531
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Glu Leu Ala Gln Arg Ala Ala Val Val Ile Glu Gly Lys Val His Pro
    75                  80                  85

CAG CGG CGG CAG CAG GGG GCA CTC GAC AGG AAG GCG GCG GCG GCG GCG        579
Gln Arg Arg Gln Gln Gly Ala Leu Asp Arg Lys Ala Ala Ala Ala Ala
    90                  95                  100                 105

GGC GAG GCA GGG GCG TGG GGC GGC GAT CGC GAG CCG CCA GCC GCG GGC        627
Gly Glu Ala Gly Ala Trp Gly Gly Asp Arg Glu Pro Pro Ala Ala Gly
                110                 115                 120

CCA CGG GCG CTG GGG CCG CCC GCC GAG GAG CCG CTG CTC GCC GCC AAC        675
Pro Arg Ala Leu Gly Pro Pro Ala Glu Glu Pro Leu Leu Ala Ala Asn
                125                 130                 135

GGG ACC GTG CCC TCT TGG CCC ACC GCC CCG GTG CCC AGC GCC GGC GAG        723
Gly Thr Val Pro Ser Trp Pro Thr Ala Pro Val Pro Ser Ala Gly Glu
            140                 145                 150

CCC GGG GAG GAG GCG CCC TAT CTG GTG AAG GTG CAC CAG GTG TGG GCG        771
Pro Gly Glu Glu Ala Pro Tyr Leu Val Lys Val His Gln Val Trp Ala
        155                 160                 165

GTG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG CTC ACC GTG CGC CTG        819
Val Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu
170                 175                 180                 185

GGG ACC TGG GGC CAC CCC GCC TTC CCC TCC TGC GGG AGG CTC AAG GAG        867
Gly Thr Trp Gly His Pro Ala Phe Pro Ser Cys Gly Arg Leu Lys Glu
                190                 195                 200

GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAC GCC AAC AGC ACC AGC        915
Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Asp Ala Asn Ser Thr Ser
            205                 210                 215

CGC GCG CCG GCC GCC TTC CGA GCC TCT TTC CCC CCT CTG GAG ACG GGC        963
Arg Ala Pro Ala Ala Phe Arg Ala Ser Phe Pro Pro Leu Glu Thr Gly
            220                 225                 230

CGG AAC CTC AAG AAG GAG GTC AGC CGG GTG CTG TGC AAG CGG TGC GCC        1011
Arg Asn Leu Lys Lys Glu Val Ser Arg Val Leu Cys Lys Arg Cys Ala
    235                 240                 245

TTG CCT CCC CAA TTG AAA GAG ATG AAA AGC CAG GAA TCG GCT GCA GGT        1059
Leu Pro Pro Gln Leu Lys Glu Met Lys Ser Gln Glu Ser Ala Ala Gly
250                 255                 260                 265

TCC AAA CTA GTC CTT CGG TGT GAA ACC AGT TCT GAA TAC TCC TCT CTC        1107
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
                270                 175                 180

AGA TTC AAG TGG TTC AAG AAT GGG AAT GAA TTG AAT CGA AAA AAC AAA        1155
Arg Phe Lys Trp Phe Lys Asn Gly Asn Glu Leu Asn Arg Lys Asn Lys
            185                 190                 195

CCA CAA AAT ATC AAG ATA CAA AAA AAG CCA GGG AAG TCA GAA CTT CGC        1203
Pro Gln Asn Ile Lys Ile Gln Lys Lys Pro Gly Lys Ser Glu Leu Arg

        200                 205                 210

ATT AAC AAA GCA TCA CTG GCT GAT TCT GGA GAG TAT ATG TGC AAA GTG        1251
Ile Asn Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val
    215                 220                 225
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ATC AGC AAA TTA GGA AAT GAC AGT GCC TCT GCC AAT ATC ACC ATC GTG    1299
Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val
230                     235             240                 245

GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA    1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val
                250             255                 260

AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC    1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
                265             270                 275

TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC    1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            280             285                 290

CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC    1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
            295             300             305

TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA                1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
400                 405             410

TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT    1590

AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA    1650

TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT    1710

AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT    1770

AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA    1830

TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA    1890

AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT    1950

CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA AAA          2003



(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     22:

     (i)  SEQUENCE CHARACTERISTICS:

          (A)  LENGTH;            12
          (B)  TYPE:              amino acid
          (C)  STRANDEDNESS:
          (D)  TOPOLOGY:          linear

     (ix)  FEATURE:

          (D)  OTHER INFORMATION:  Xaa in position 11 is unknown.

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
 1               5                   10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 11
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 9 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys

  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys

  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 7 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 10
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 9
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ala Lys Glu Ala Leu Ala Ala Leu Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 7
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe Val Leu Gln Ala Lys Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 21
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
  1   5   10   15

Ile Gly Ala Tyr Thr
                20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 21
                (B) TYPE: amino acid
                (C) STRANDEDNESS:
                (D) TOPOLOGY: linear

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(ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is
unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys Glu
  1   5   10   15

Xaa Gly Xaa Gly Lys
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 6 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Argininel; Xaa in position 11 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly

 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 14
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 13 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr

 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 7
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 1 is Lysine or
Arginine; Xaa in position 6 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
 1   5

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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 39
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
 1   5   10   15

Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
            20   25   30

Thr Cys Thr Cys Ala Gly Cys
            35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 24
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
 1   5   10   15

Thr Gly Cys Cys Cys Thr Thr Cys
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 60
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 36
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG   36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 569
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAGGCGGAGG AGCTGTACCA GAAGAGAGTG CTGACCATAA CCGGCATCTG CATCGCCCTC 60

CTTGTGGTCG GCATCATGTG TGTGGTGGCC TACTGCAAAA CCAAGAAACA GCGGAAAAAG 120

CTGCATGACC GTCTTCGGCA GAGCCTTCGG TCTGAACGAA ACAATATGAT GAACATTGCC 180

AATGGGCCTC ACCATCCTAA CCCACCCCCC GAGAATGTCC AGCTGGTGAA TCAATACGTA 240

TCTAAAAACG TCATCTCCAG TGAGCATATT GTTGAGAGAG AAGCAGAGAC ATCCTTTTCC 300

ACCAGTCACT ATACTTCCAC AGCCCATCAC TCCACTACTG TCACCCAGAC TCCTAGCCAC 360

AGCTGGAGCA ACGGACACAC TGAAAGCATC CTTTCCGAAA GCCACTCTGT AATCGTGATG 420

TCATCCGTAG AAAACAGTAG GCACAGCAGC CCAACTGGGG GCCCAAGAGG ACGTCTTAAT 480

GGCACAGGAG GCCCTCGTGA ATGTAACAGC TTCCTCAGGC ATGCCAGAGA AACCCCTGAT 540

TCCTACCGAG ACTCTCCTCA TAGTGAAAG   569

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Val His Gln Val Trp Ala Ala Lys
  1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 8
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 9
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 6
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in position 5 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:

    (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

      (ix) FEATURE:

             (D) OTHER INFORMATION: N at positions 3, 12 and 18 is C
or T; N at position 6 is A or G; N at positions 9 and 15 is A, T,
G or C.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTNAANGGNG ANGCNCANAC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:

      (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 21
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

      (ix) FEATURE:

             (D) OTHER INFORMATION: N at positions 7 and 13 is C or T;
N at positions 4, 10, and 16 is A or G; N at position 19 is A, T, G
or C.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATNTANTCN TANTCNTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:

      (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 20
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

      (ix) FEATURE:

             (D) OTHER INFORMATION: N at positions 3 and 15 is C or T;
N at positions 6, 9, and 18 is A, T, G or C.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGNTCNGANG CCATNTCNGT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:

      (i) SEQUENCE CHARACTERISTICS:

             (A) LENGTH: 20
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear

(ix)   FEATURE:

        (D)   OTHER INFORMATION: N at positions 3 and 14 is C or T;
N at position 6 is A or G; N at positions 9 and 17 is A, T, G or C.

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGNTCNCTNG CCATNTCNGT   20

(2)   INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:

    (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 20
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

    (ix)   FEATURE:

        (D)   OTHER INFORMATION: N at position 3 is A, G or T; N
at position 18 is C or T; N at positions 6, 12, and 15 is A, T,
G or C.

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCNATNACCA TNGGNACNTT   20

(2)   INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:

    (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 20
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

    (ix)   FEATURE:

        (D)   OTHER INFORMATION: N at position 12 is C or T; N at
position 15 is A or G; N at positions 3, 9 and 18 is A, T, G or C.

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCANA CYTGRTGNAC   20

(2)   INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60:

    (i)   SEQUENCE CHARACTERISTICS:

            (A)   LENGTH: 20
            (B)   TYPE: nucleic acid
            (C)   STRANDEDNESS: single
            (D)   TOPOLOGY: linear

    (ix)   FEATURE:

        (D)   OTHER INFORMATION: N at positions 3 and 9 is C or T;
N at positions 5 and 8 is A or G; N at position 6 is A, T, G or C.

    (xi)   SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCNTCNGGNT CCATNAANAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at position 6 is A, G or T; N at
position 3 is C or T; N at position 15 is A or G; N at positions 9
and 11 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCNTCNATNA CNACNAACCA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 6 and 9 is A or G;
N at positions 3, 11 and 14 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCNAANT ANCCNGC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 12 and 15 is C or T;
N at positions 3, 6, 9 and 17 is A, T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CNTCNTTNGC   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:

    (i) SEQUENCE CHARACTERISTICS:

```
          (A)  LENGTH:              20
          (B)  TYPE:                nucleic acid
          (C)  STRANDEDNESS:        single
          (D)  TOPOLOGY:            linear

     (ix)  FEATURE:

          (D)  OTHER INFORMATION:  N at positions 6, 12 and 15 is C or T;
N at positions 3, 9, and 18 is A, T, G or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCNAANG CNTCNTTNGC                                              20


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     65:

     (i) SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:              20
          (B)  TYPE:                nucleic acid
          (C)  STRANDEDNESS:        single
          (D)  TOPOLOGY:            linear

     (ix)  FEATURE:

          (D)  OTHER INFORMATION:  N at positions 3 and 9 is C or T;
N at position 18 is A or G; N at positions 6, 12 and 15 is A, T, G
or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:


TTNTTNGCNT GNAGNACNAA                                              20


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     66:

     (i) SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:              20
          (B)  TYPE:                nucleic acid
          (C)  STRANDEDNESS:        single
          (D)  TOPOLOGY:            linear

     (ix)  FEATURE:

          (D)  OTHER INFORMATION:  N at positions 3, 9 and 12 is C or T;
N at position 18 is A or G; N at positions 6 and 15 is A, T, G or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTNTTNGCNT GNAANACNAA                                              20


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     67:

     (i) SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:              17
          (B)  TYPE:                nucleic acid
          (C)  STRANDEDNESS:        single
          (D)  TOPOLOGY:            linear

     (ix)  FEATURE:
```

(D) OTHER INFORMATION: N at positions 9 and 12 is C or T; N at positions 3, 6 and 15 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGNT CNTGNAC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68:

(i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 17 .
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 6, 9, and 12 is C or T; N at positions 3 and 15 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACNAANT CNTGNAC   17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69:

(i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at position 7 is C or T; N at positions 4 and 16 is A or G; N at positions 10, 13 and 19 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATNTANTCN CCNGANTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:

(i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at position 7 is C or T; N at positions 4, 13 and 16 is A or G; N at positions 10 and 19 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATNTANTCN CCNCTNTCNG C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 10 and 19 is C or T;
N at position 4 is A or G; N at positions 1, 7, 13 and 16 is A, T,
G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGANTCNGCN AANGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at position 19 is C or T; N at
position 4 is A or G; N at positions 1, 7, 10, 13 and 16 is A, T,
G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGANTCNGCN AGNGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 21
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N at positions 10 and 19 is C or T;
N at positions 1 and 4 is A or G; N at positions 7, 13 and 16 is A,
T, G or C.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

NCTNTCNGCN AANGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:

(i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 21
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:

            (D) OTHER INFORMATION: N at position 19 is C or T; N at
positions 1 and 14 is A or G; N at positions 7, 10, 13 and 16 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

NCTNTCNGCN AGNGANGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 21
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:

            (D) OTHER INFORMATION: N at positions 10 and 19 is C or T;
N at positions 4 and 13 is A or G; N at positions 1, 7 and 16 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGANTCNGCN AANCTNGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 21
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:

            (D) OTHER INFORMATION: N at position 19 is C or T; N at
positions 4 and 13 is A or G; N at positions 1, 7, 10 and 16 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGANTCNGCN AGNCTNGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 730
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single

```
              (D) TOPOLOGY:              linear

      (ix)  FEATURE:

            (D)   OTHER INFORMATION:

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTCC ACACGCCAAG  60

CTCCCCCAAA TCGCCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT 120

GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTGACACC 180

ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCTCAG CAGTTCAGCT CCTTCCACCA 240

CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA 300

GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA 360

TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA 420

CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACAGAAGATG AAAGAGTAGG 480

TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCCTGGCA GCCAGTCTTG AGGCAACACC 540

TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCAGCAGGC CGCTTCTCGA CACAGGAAGA 600

AATCCAGGCC AGGCTGTCTA GTGTAATTGC TAACCAAGAC CCTATTGCTG TATAAAACCT 660

AAATAAACAC ATAGATTCAC CTGTAAAACT TTATTTTATA TAATAAAGTA TTCCACCTTA 720

AATTAAACAA                                                       730


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    78:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH:                21
            (B) TYPE:                  nucleic acid
            (C) STRANDEDNESS:          single
            (D) TOPOLOGY:              linear

      (ix)  FEATURE:

            (D)   OTHER INFORMATION:  N at positions 10 and 19 is C or
T; N at positions 1, 4 and 13 is A or G; N at positions 7 and 16
is A, T, G or C.

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

NCTNTCNGCN AANCTNGCNT T                                           21


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    79:

      (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH:                21
            (B) TYPE:                  nucleic acid
            (C) STRANDEDNESS:          single
            (D) TOPOLOGY:              linear

      (ix)  FEATURE:
```

(D) OTHER INFORMATION: N at position 19 is C or T; N at positions 1, 4 and 13 is A or G; N at positions 7, 10 and 16 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

NCTNCTNGCN AGNCTNGCNT T   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:

(i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

(ix) FEATURE:

          (D) OTHER INFORMATION: N at position 9 is A or G; N at positions 3, 6, 17 and 18 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGANA TGGCTCNNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:

(i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

(ix) FEATURE:

          (D) OTHER INFORMATION: N at position 16 is C or T; N at position 9 is A or G; N at positions 3, 6 and 17 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGANA TGGCAGNNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:

(i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

(ix) FEATURE:

          (D) OTHER INFORMATION: N at position 3 is C or T; N at position 6 is A or G; N at positions 9, 15 and 18 is A, T, G or C.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CANCANGTNT GGGCNGCNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D) OTHER INFORMATION: N at position 3 is C or T; N at
position 15 is A or G; N at positions 9, 15 and 18 is A, T, G or
C; N at position 12 is A, C or T.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTNGTNGTNA TNGANGGNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D) OTHER INFORMATION: N at positions 9 and 15 is C or T;
N at position 3 is A or G; N at positions 6, 12 and 18 is A, T, G
or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AANGGNGANG CNCANACNGA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 20
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D) OTHER INFORMATION: N at positions 7 and 15 is C or T;
N at position 3 is A or G; N at positions 6, 9, 11, 14 and 17 is
A, T, G or C.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GANGCNNTNG CNGCNNTNAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:

(i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N at position 19 is C or T; N at
positions 15 and 18 is A or G; N at positions 3, 6, 9 and 12 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNGGNTCNG TNCANGANNT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N at positions 9 and 19 is C or T;
N at positions 15 and 18 is A or G; N at positions 3, 6 and 12 is
A, T, G or C.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNGGNAGNG TNCANGANNT   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 21
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N at positions 4, 7 and 16 is C
or T; N at position 12 is A or G; N at positions 1, 10 and 19 is
A, T, G or C; N at position 13 is A, G or T.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACNTTNTTN ANNATNTGNC C   21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 417
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single

```
        (D) TOPOLOGY:              linear
    (ix) FEATURE:

        (D)  OTHER INFORMATION:  Xaa in positions 14, 23, 90, 100, 126,
and 135 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA 53
      Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile
      1               5                   10                  15

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT      101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile
        20          25                  30

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC      149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile
        35          40                  45

AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG      197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu
        50          55                  60

TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA      245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg
65              70              75              80

GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TCT GAA      293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Ser Glu
            85              90              95

ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG      341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu
        100             105             110

AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA      389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu
        115             120             125

ATA GAC CTG AAA TAT ATA TAG ATT ATT T                                417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile
        130             135

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    90:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH:               33
        (B) TYPE:                 nucleic acid
        (C) STRANDEDNESS:         single
        (D) TOPOLOGY:             linear

    (ix) FEATURE:

        (D)  OTHER INFORMATION:  N in position 16 can be A or G; N
in position 22 can be A or G; N in position 28 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGANACUC ANCCUGANCC UGG                            33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    91:
```

(i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 37
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N in position 17 can be A or G; N in
position 26 can be A, G or T.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGUGTNTAU GCUCCNATUA CCATUGG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 34
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N in position 19 can be C or T; N in
position 28 can be A or G; N in position 31 can be C or T.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCUGANT CUGGUGANTA NATG   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 33
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

        (ix) FEATURE:

                (D) OTHER INFORMATION: N in position 19 can be C or T; N in
position 22 can be C or T; N in position 28 can be A or G; N in position
31 can be C or T.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCUGANA GNGGUGANTA NAT   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 94:

        (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 34
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single

132

(D) TOPOLOGY: linear

     (ix) FEATURE:

          (D)   OTHER INFORMATION: N in position 19 can be A or G; N in
position 22 can be C or T; N in position 32 can be A or G.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGUUUCATN TANTCUCCUG ANTC   34

     (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 95:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 34
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D)   OTHER INFORMATION: N in position 20 can be A or G; N in
position 23 can be C or T; N in position 29 can be A or G; N in
position 32 can be A or G.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGGATCCTG CAGUUUCATN TANTCUCCNC TNTC   34

     (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 33
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ix) FEATURE:

          (D)   OTHER INFORMATION: N in position 16 can be C or T; N in
position 19 can be A or G.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCANCANG TUTGGGCUGC TAA   33

     (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 35
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

     (ix) FEATURE:

133

(D)   OTHER INFORMATION: N in position 16 can be A or C or T;
N in position 19 can be C or T; N in position 22 can be C or T; N in
position 28 can be A or G; N in position 34 can be A or G.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATNTTNT TNATGGANCC UGANG   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 35
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:

            (D)   OTHER INFORMATION: N in position 30 can be C or T.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAATTCTG CAGGGGGUCC UCCUGCUTTN CCUGT   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 33
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:

            (D)   OTHER INFORMATION: N in position 19 can be C or T; N in
position 28 can be A or C or T; N in position 31 can be A or G.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTNG TUGTUATNGA NGG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:

        (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 34
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ix) FEATURE:

            (D)   OTHER INFORMATION: N at position 17, 20, and 26 is
Inosinc. Y can be cytidine or thymidine.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGC NGCCCANACY TGRTG   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 16 can be C or T; N in
position 22 can be C or T; N in position 28 can be A or G; N in position
31 can be A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCNTCUG GNTCCATNAA NAA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 19 can be A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACUGGNA AUGCUGGUGG UCC   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 14 can be C or T; N in
position 20 can be C or T; N in position 23 can be A or G or T; N in
position 32 can be A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGNTTUCCN TCNATUACUA CNAAC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 4 can be A or G; N in
position 7 cna be C or T; N in position 10 can be A or G; N in position
13 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATNTANTCN TANTCTCUGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 16 can be A or G; N
in position 22 can be C or T; N in position 28 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAANGGUG ANGCUCANAC UGA   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 6 can be C or T; N in
position 12 can be C or T; N in position 15 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCUGCNAAUG CNTCNTTUGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 33
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 12 can be C or T; N in
position 15 can be C or T.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCUGCUAGUG CNTCNTTTGC AAGGATCCTG CAG   33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 30
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 6 can be A or G; N in
position 9 can be A or G.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCUGCNAANT AUCCUGCAAG GATCCTGCAG   30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 38
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA   38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 37
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG   37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 34
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA   34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 35
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC   35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:

    (i) SEQUENCE CHARACTERISTICS:

```
            (A)  LENGTH:              33
            (B)  TYPE:                nucleic acid
            (C)  STRANDEDNESS:        single
            (D)  TOPOLOGY:            linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA                          33


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    117:

     (i)  SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:              39
            (B)  TYPE:                nucleic acid
            (C)  STRANDEDNESS:        single
            (D)  TOPOLOGY:            linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTCAC ACACCTGCG                    39


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    118:

     (i)  SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:              36
            (B)  TYPE:                nucleic acid
            (C)  STRANDEDNESS:        single
            (D)  TOPOLOGY:            linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGAA CCTGCCACAG ACTCCT                       36


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    119:

     (i)  SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:              39
            (B)  TYPE:                nucleic acid
            (C)  STRANDEDNESS:        single
            (D)  TOPOLOGY:            linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATACCCGGGC TGCAGATGAG ATTTCACACA CCTGCGTGA                    39


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    120:

     (i)  SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:              12
            (B)  TYPE:                amino acid
            (C)  STRANDEDNESS:
            (D)  TOPOLOGY:            linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 120:
```

139

```
His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
  1               5                   10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

```
Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
  1           5                   10                  15
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 12 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

```
Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
  1               5                   10
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 23
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

```
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
  1           5                   10                  15

Cys Gly Arg Leu Lys Glu Asp
              20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 13
        (B) TYPE: amino acid
        (C) STRANDEDNESS:

(D) TOPOLOGY: linear

     (ix) FEATURE:

          (D)   OTHER INFORMATION: Xaa in position 10 is unknown.

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 23
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
 1   5   10   15

Ser Gly Gly Pro Gly Arg Leu
           20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 14
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:

     (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 16
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1   5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:

     (i) SEQUENCE CHARACTERISTICS:

141

```
        (A)  LENGTH:              26
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
 1               5                  10                  15

Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            20                  25


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     129:

   (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              13
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

   (ix)  FEATURE:

        (D)   OTHER INFORMATION:  Xaa in position 12 is unknown.

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
 1               5                  10


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     130:

   (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              23
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
 1               5                  10                  15

Cys Lys Val Ile Ser Lys Leu
            20


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     131:

   (i)  SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:              12
        (B)  TYPE:                amino acid
        (C)  STRANDEDNESS:
        (D)  TOPOLOGY:            linear

   (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1               5                  10
```

142

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 22
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

```
Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
 1           5                  10                  15

Lys Val Ile Ser Lys Leu
            20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 744
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
         1           5                  10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
         20                  25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
         35                  40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 199
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
         50                  55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
                100             105             110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
        115                 120                 125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
    130                 135                 140
```

```
TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT  487
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145                 150                 155                 160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC  535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                165                 170                 175

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT  583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile
            180                 185                 190

TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT          625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr
            195                 200                 205

TGAATCACGC AGGTGTGTGA AATCTCATTG TCAACAAATA AAAATCATGA AAGGAAAAAA 685

AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC  744


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    134:

     (i)  SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:              1193
          (B)  TYPE:                nucleic acid
          (C)  STRANDEDNESS:        single
          (D)  TOPOLOGY:            linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 55
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
        1               5                   10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20              25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
            35              40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
            50              55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100                 105                 110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 391
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
            115                 120                 125
```

144

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 439
Arg Lys Asn Lys Gly Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
    130   135   140

TCA GGA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 487
Ser Gly Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145   150   155   160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 535
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                  165   170   175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA 583
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
                  180   185   190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 631
Ser His Leu Val Lys Ser Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
                  195   200   205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
    210   215   220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 727
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225   230   235   240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AGT GCC CAA ATG AGT TTA CTG 775
Val Pro Met Lys Val Gln Thr Gln Glu Ser Ala Gln Met Ser Leu Leu
                  245   250   255

GTG ATC GCT GCC AAA ACT ACG TAA GGCCAG CTTCTACAGT ACGTCCACTC   826
Val Ile Ala Ala Lys Thr Thr
                  260

CCTTTCTGTC TCTGCCTGAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC 886

TCCCCTCAGA TTCCTCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT 946

GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT 1006

GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT 1066

ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA 1126

GTCAAAAAAA AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT GCAGGTCGAC 1186

TCTAGAG   1193

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135:

        (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1108 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: cDNA
       (ix) FEATURE:

          (A) NAME/KEY: Coding Sequence
          (B) LOCATION: 8...778
          (D) OTHER INFORMATION:

145

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

```
CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC    49
        His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp
        1               5               10

TCG CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC    97
Ser Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro
15              20              25              30

TCC TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG   145
Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu
            35              40              45

CCC GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT   193
Pro Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu
            50              55              60

CCC CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT   241
Pro Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly
            65              70              75

GCT GTG CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT   289
Ala Val Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser
    80              85              90

CAG GAG TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT   337
Gln Glu Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser
95              100             105             110

TCT GAA TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA   385
Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu
            115             120             125

TTA AGC CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG   433
Leu Ser Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro
            130             135             140

GGG AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA   481
Gly Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
            145             150             155

GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT   529
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
    160             165             170

GCC AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT   577
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala
175             180             185             190

GGG ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT   625
Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys
            195             200             205

GTG AAT GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA   673
Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser
            210             215             220

AGA TAC TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA   721
Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln
            225             230             235

AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT   769
Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser
```

146

```
         240                 245                 250

CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAG 827
Leu Pro Glu
255

ATTCCGCCTA GAGCTAGATG CGTTTTACCA GGTCTAACAT TGACTGCCTC TGCCTGTCGC  887
ATGAGAACAT TAACACAAGC GATTGTATGA CTTCCTCTGT CCGTGACTAG TGGGCTCTGA  947
GCTACTCGTA GGTGCGTAAG GCTCCAGTGT TTCTGAAATT GATCTTGAAT TACTGTGATA 1007
CGACATGATA GTCCCTCTCA CCCAGTGCAA TGACAATAAA GGCCTTGAAA AGTCAAAAAA 1067
AAAAAAAAAA AAAAAATCGA TGTCGACTCG AGATGTGGCT G                     1108
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 559
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: N in position 214 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

```
AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC  60

GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC 120

TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC 180

CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC 240

AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCCGCCGGC GACAGGAGAC 300

GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC 360

AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC 420

CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA      474
                                          Met Ser Glu Arg Arg
                                           1               5

GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG    522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly
                  10              15                  20

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G                  559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala
              25              30
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 252
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

147

(ix) FEATURE:

            (D)   OTHER INFORMATION: N in position 8 could be either
A or G.

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG   47
   His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser
    1   5   10   15

CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC   95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
            20   25   30

TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC   143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro
            35   40   45

GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC   191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro
            50   55   60

CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT   239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala
    65   70   75

GTG CAA CGG TGC G   252
Val Gln Arg Cys
 80

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 178
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG   48
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly
 1   5   10   15

GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC   96
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu
            20   25   30

TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA   144
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
            35   40   45

AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G   178
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly
    50   55

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:

    (i) SEQUENCE CHARACTERISTICS:

```
        (A)  LENGTH:                122
        (B)  TYPE:                  nucleic acid
        (C)  STRANDEDNESS:          single
        (D)  TOPOLOGY:              linear



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA      46
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly
   1               5                   10                  15

GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT   94
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser
                20                  25                  30

GCC AAC ATC ACC ATT GTG GAG TCA AAC G                             122
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala
            35


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    140:

    (i) SEQUENCE CHARACTERISTICS:

        (A)  LENGTH:                417
        (B)  TYPE:                  nucleic acid
        (C)  STRANDEDNESS:          single
        (D)  TOPOLOGY:              linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTAAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC  60

CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG     110
                         Lys Ser Glu Leu Arg Ile Ser Lys Ala
                          1                   5

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA   158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
 10                  15                  20                  25

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT   206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly
                30                  35                  40

AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC   254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile
                45                  50                  55

AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG          302
Lys Val Cys Gly His Thr
                60


TGAACAAATA AAAATCATGA AAGGAAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT 362

GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT       417


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    141:
```

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 102
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

```
 AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT      47
 Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
 1               5               10              15

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT      95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
            20              25              30

TCT TCA T                                                           102
Ser Ser Ser
        35
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 69
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

```
AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC      48
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu·Asn Val Pro
 1               5               10              15

ATG AAA GTC CAA ACC CAA GAA                                          69
Met Lys Val Gln Thr Gln Glu
            20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 60
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

```
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG      48
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met ·
 1               5               10              15

GCC AGC TTC TAC                                                      60
Ala Ser Phe Tyr
```

150

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 36
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG   36
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 27
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

AAG CAT CTT GGG ATT GAA TTT ATG GAG   27
Lys His Leu Gly Ile Glu Phe Met Glu
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 569
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT   48
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
 1   5   10   15

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC   96
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
           20   25   30

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC   144
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
        35   40   45

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC   192
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
   50   55   60

```
CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA        240
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
65                  70                  75                  80

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG        288
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
                85                  90                  95

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT        336
Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
            100                 105                 110

ACT GTC ACT CAG ACT CCC AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA        384
Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His Thr Glu
            115                 120                 125

AGC ATC ATT TCG GAA AGC CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA        432
Ser Ile Ile Ser Glu Ser His Ser Val Ile Val Met Ser Ser Val Glu
        130                 135                 140

AAC AGT AGG CAC AGC AGC CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT        480
Asn Ser Arg His Ser Ser Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn
145                 150                 155                 160

GGC TTG GGA GGC CCT CGT GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA        528
Gly Leu Gly Gly Pro Arg Glu Cys Asn Ser Phe Leu Arg His Ala Arg
                165                 170                 175

GAA ACC CCT GAC TCC TAC CGA GAC TCT CCT CAT AGT G AAAG               569
Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser
            180                 185


(2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     147:

     (i)  SEQUENCE CHARACTERISTICS:

          (A)  LENGTH:              730
          (B)  TYPE:                nucleic acid
          (C)  STRANDEDNESS:        single
          (D)  TOPOLOGY:            linear

     (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 147:


G TAT GTA TCA GCA ATG ACC ACC CCG GCT CGT ATG TCA CCT GTA GAT          46
  Tyr Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp
  1               5                   10                  15

TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC CCT TCG GAA ATG TCC CCG        94
Phe His Thr Pro Ser Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro
            20                  25                  30

CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC TCC ATG GCG GTC AGT CCC       142
Pro Val Ser Ser Thr Thr Val Ser Met Pro Ser Met Ala Val Ser Pro
            35                  40                  45

TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT GTG ACG CCA CCA CGG CTG       190
Phe Val Glu Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu
        50                  55                  60

CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA TTC AAC TCG TTC CAC TGC       238
Arg Glu Lys Tyr Asp His His Ala Gln Gln Phe Asn Ser Phe His Cys
    65                  70                  75
```

```
AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG ATA    286
Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile
 80                      85                  90              95

GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT CAA    334
Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln
                    100                 105             110

GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA ACC    382
Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg Thr
                115                 120             125

AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC ACA    430
Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn Thr
            130                 135             140

GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA GTA    478
Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val
    145                 150             155

GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC AGT    526
Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala Ser
160                 165             170                 175

CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC CCA    574
Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn Pro
                180             185                 190

ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC GGT    622
Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser Gly
            195             200                 205

GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAAAACCGAA ATACACCCAT      672
Val Ile Ala Asn Gln Asp Pro Ile Ala Val
            210             215

AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAAACAA    730


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    148:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1652 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: cDNA
        (ix) FEATURE:

            (A) NAME/KEY: Coding Sequence
            (B) LOCATION: 459...1181
            (D) OTHER INFORMATION:

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC   60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC  120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC  180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGCGTGCGA CCGGGACGGA GCGCCCGCCA  240
GTCCCAGGTG GCCCGGACCG CACGTTGCGT CCCCGCGCTC CCCGCCGGCG ACAGGAGACG  300
CTCGCCCCCA CGCCGCGCGC GCCTCGGCCC GGTCGCTGGC CCGCCTCCAC TCCGGGGACA  360
AACTTTTCCC GAAGCCGATC CCAGCCCTCG ACCCAAACT TGTCGCGCGT CGCCTTCGCC  420
```

153

GGGAGCCGTC CGCGCAGAGC GTGCACTTCT CGGGCGAG ATG TCG GAG CGC AGA GAA 476
                                                 Met Ser Glu Arg Arg Glu
                                                    1   5

GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG AAG 524
Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly Lys
           10   15   20

AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC CGC 572
Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro Arg
           25   30   35

TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA GTG 620
Leu Lys Glu Met Lys Met Gln Glu Ser Val Ala Gly Ser Lys Leu Val
55

CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG TGG 668
Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp
55   60   65   70

TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC ATC 716
Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys Pro Gln Asn Ile
                       75   80   85

AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA GCG 764
Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys Ala
                       90   95   100

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA 812
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
                       105   110   115

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GAG 860
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Glu
                       120   125   130

ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT TCA 908
Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser Ser
135   140   145   150

GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT TCT 956
Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr Ser
                       155   160   165

TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT 1004
Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys
                       170   175   180

GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG 1052
Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met
                       185   190   195

GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA AAT 1100
Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn
                       200   205   210

GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC 1148
Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr
215   220   225   230

AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG CTCAGTCGGT 1201
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
                       235   240

GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT GCGTTTTACC 1261

```
AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG CGATTGTATG 1321
ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA GGCTCCAGTG 1381
TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC ACCCAGTGCA 1441
ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAT CGTTCCACGG 1501
GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG TTAAGTTGTA 1561
ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT TCTTTCTGAC 1621
AAATAAACAG AATAAAAAAA AAAAAAAAAA A                                1652
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 1140
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG 48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu
1               5                   10                  15

CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC 96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys
            20                  25                  30

GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG 144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu
        35                  40                  45

GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC 192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro
    50                  55                  60

TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG 240
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val
65                  70                  75                  80

CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG 288
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu
                85                  90                  95

TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA 336
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu
            100                 105                 110

TAC TCC TCT CTC AAG TTC AAG TGG TTC AAG AAT GGG AGT GAA TTA AGC 384
Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser
        115                 120                  125

CGA AAG AAC AAA CCA GAA AAC ATC AAG ATA CAG AAA AGG CCG GGG AAG 432
Arg Lys Asn Lys Pro Glu Asn Ile Lys Ile Gln Lys Arg Pro Gly Lys
    130                 135                 140

TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT 480
Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr
145                 150                 155                 160

ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC 528
Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn
                165                 170                 175

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA 576
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
```

```
Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr
        180              185              190

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 624
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
        195              200              205

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 672
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
    210              215              220

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 720
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
225              230              235              240

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 768
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
            245              250              255

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 816
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
            260              265              270

ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG 870
Thr Pro Phe Leu Ser Leu Pro Glu
            275              280

TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT 930

GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC 990

CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG 1050

ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG 1110

GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA                                 1140


    (2)  INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    150:

        (i) SEQUENCE CHARACTERISTICS:

            (A)  LENGTH:               1764
            (B)  TYPE:                 nucleic acid
            (C)  STRANDEDNESS:         single

            (D)  TOPOLOGY:             linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:


G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA   49
  Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu
   1            5               10              15

TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC   97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala
        20              25              30

AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG  145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly
        35              40              45

ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG  193
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Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val
    50                  55                  60

AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA    241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg
65                  70                  75                  80

TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG    289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu
                85                  90                  95

AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC    337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
                100                 105                 110

CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG    385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val
            115                 120                 125

GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC AAA ACC AAG AAA CAA CGG    433
Val Gly Ile Met Cys Val Val Val Tyr Cys Lys Thr Lys Lys Gln Arg
            130                 135                 140

AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC CTT CGG TCT GAA AGA AAC    481
Lys Lys Leu His Asp Arg Leu Arg Gln Ser Leu Arg Ser Glu Arg Asn
145                 150                 155                 160

ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC CAC CCC AAT CCG CCC CCC    529
Thr Met Met Asn Val Ala Asn Gly Pro His His Pro Asn Pro Pro Pro
                165                 170                 175

GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA TCT AAA AAT GTC ATC TCT    577
Glu Asn Val Gln Leu Val Asn Gln Tyr Val Ser Lys Asn Val Ile Ser
                180                 185                 190

AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG AGC TCT TTT TCC ACC AGT    625
Ser Glu His Ile Val Glu Arg Glu Ala Glu Ser Ser Phe Ser Thr Ser
                195                 200                 205

CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT ACT GTC ACT CAG ACT CCC    673
His Tyr Thr Ser Thr Ala His His Ser Thr Thr Val Thr Gln Thr Pro
    210                 215                 220

AGT CAC AGC TGG AGC AAT GGA CAC ACT GAA AGC ATC ATT TCG GAA AGC    721
Ser His Ser Trp Ser Asn Gly His Thr Glu Ser Ile Ile Ser Glu Ser
225                 230                 235                 240

CAC TCT GTC ATC GTG ATG TCA TCC GTA GAA AAC AGT AGG CAC AGC AGC    769
His Ser Val Ile Val Met Ser Ser Val Glu Asn Ser Arg His Ser Ser
                245                 250                 255

CCG ACT GGG GGC CCG AGA GGA CGT CTC AAT GGC TTG GGA GGC CCT CGT    817
Pro Thr Gly Gly Pro Arg Gly Arg Leu Asn Gly Leu Gly Gly Pro Arg
            260                 265                 270

GAA TGT AAC AGC TTC CTC AGG CAT GCC AGA GAA ACC CCT GAC TCC TAC    865
Glu Cys Asn Ser Phe Leu Arg His Ala Arg Glu Thr Pro Asp Ser Tyr
        275                 280                 285

CGA GAC TCT CCT CAT AGT GAA AGA CAT AAC CTT ATA GCT GAG CTA AGG    913
Arg Asp Ser Pro His Ser Glu Arg His Asn Leu Ile Ala Glu Leu Arg
    290                 295                 300

AGA AAC AAG GCC CAC AGA TCC AAA TGC ATG CAG ATC CAG CTT TCC GCA    961
```

Arg Asn Lys Ala His Arg Ser Lys Cys Met Gln Ile Gln Leu Ser Ala
305   310   315   320

ACT CAT CTT AGA GCT TCT TCC ATT CCC CAT TGG GCT TCA TTC TCT AAG   1009
Thr His Leu Arg Ala Ser Ser Ile Pro His Trp Ala Ser Phe Ser Lys
                325   330   335

ACC CCT TGG CCT TTA GGA AGG TAT GTA TCA GCA ATG ACC ACC CCG GCT   1057
Thr Pro Trp Pro Leu Gly Arg Tyr Val Ser Ala Met Thr Thr Pro Ala
                340   345   350

CGT ATG TCA CCT GTA GAT TTC CAC ACG CCA AGC TCC CCC AAG TCA CCC   1105
Arg Met Ser Pro Val Asp Phe His Thr Pro Ser Ser Pro Lys Ser Pro
            355   360   365

CCT TCG GAA ATG TCC CCG CCC GTG TCC AGC ACG ACG GTC TCC ATG CCC   1153
Pro Ser Glu Met Ser Pro Pro Val Ser Ser Thr Thr Val Ser Met Pro
        370   375   380

TCC ATG GCG GTC AGT CCC TTC GTG GAA GAG GAG AGA CCC CTG CTC CTT   1201
Ser Met Ala Val Ser Pro Phe Val Glu Glu Glu Arg Pro Leu Leu Leu
385   390   395   400

GTG ACG CCA CCA CGG CTG CGG GAG AAG TAT GAC CAC CAC GCC CAG CAA   1249
Val Thr Pro Pro Arg Leu Arg Glu Lys Tyr Asp His His Ala Gln Gln
                405   410   415

TTC AAC TCG TTC CAC TGC AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC   1297
Phe Asn Ser Phe His Cys Asn Pro Ala His Glu Ser Asn Ser Leu Pro
                420   425   430

CCC AGC CCC TTG AGG ATA GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG   1345
Pro Ser Pro Leu Arg Ile Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln
            435   440   445

GAG TAC GAA CCA GCT CAA GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC   1393
Glu Tyr Glu Pro Ala Gln Glu Pro Val Lys Lys Leu Thr Asn Ser Ser
        450   455   460

CGG CGG GCC AAA AGA ACC AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG   1441
Arg Arg Ala Lys Arg Thr Lys Pro Asn Gly His Ile Ala His Arg Leu
465   470   475   480

GAA ATG GAC AAC AAC ACA GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA   1489
Glu Met Asp Asn Asn Thr Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu
            485   490   495

ACA GAG GAT GAA AGA GTA GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG   1537
Thr Glu Asp Glu Arg Val Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln
            500   505   510

AAC CCC CTG GCA GCC AGT CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC   1585
Asn Pro Leu Ala Ala Ser Leu Glu Ala Ala Pro Ala Phe Arg Leu Val
            515   520   525

GAC AGC AGG ACT AAC CCA ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG   1633
Asp Ser Arg Thr Asn Pro Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu
            530   535   540

CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC   1681
Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val
545   550   555   560

TAAAACCGAA ATACACCCAT AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT   1741

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 50
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 1   5   10   15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            20   25   30

Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
        35   40   45

Phe Tyr
    50

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 50
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 1   5   10   15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
            20   25   30

Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
        35   40   45

Val Gln
    50

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153:

    (i) SEQUENCE CHARACTERISTICS:

            (A) LENGTH: 46
            (B) TYPE: amino acid
            (C) STRANDEDNESS:
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu Cys Leu Arg Lys Tyr Lys Asp Phe Cys Ile His Gly Glu Cys Lys
 1   5   10   15

Tyr Val Lys Glu Leu Arg Ala Pro Ser Cys Lys Cys Gln Gln Glu Tyr

```
         20                    25                    30
Phe Gly Glu Arg Cys Gly Glu Lys Ser Asn Lys Thr His Ser
        35                    40                    45
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 154:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 198
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
        35                  40                  45

GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT 192
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro
    50                  55                  60

GAA TAG                                                          198
Glu
65
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 192
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
        35                  40                  45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 183
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
            35                  40                  45

GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA             183
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr
            50                  55                  60
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 210
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

```
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1               5                   10                  15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
            20                  25                  30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
            35                  40                  45

GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA 192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys
            50                  55                  60

GCG GAG GAG CTC TAC TAA                                         210
Ala Glu Glu Leu Tyr
65
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 267
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
            35   40   45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
        50   55   60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AGT ACG TCC 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser
65   70   75   80

ACT CCC TTT CTG TCT CTG CCT GAA TAG   267
Thr Pro Phe Leu Ser Leu Pro Glu
                85

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 252
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1   5   10   15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
                20   25   30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
            35   40   45

GTG CCC ATG AAA GTC CAA ACC CAA GAA AAG TGC CCA AAT GAG TTT ACT 192

162

```
Val Pro Met Lys Val Gln Thr Gln Glu Lys Cys Pro Asn Glu Phe Thr
    50                      55                  60

GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC TAC AAA GCG GAG 240
Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys Ala Glu
 65                      70              75                  80

GAG CTC TAC TAA                                                  252
Glu Leu Tyr
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 128
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

```
CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA      47
   Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala
    1           5               10                  15

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG     95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val
                20              25              30

AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC                       128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
            35              40
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 141
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

```
A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC       46
  His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser
   1           5               10                  15

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC     94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser
                20              25              30

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG     141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg
                35              40                  45
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:

    (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in positions 15 and 22 is
unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
 1   5   10   15

Met Val Lys Asp Leu Xaa Asn Pro
            20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 745
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG 48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
1   5   10   15

GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG 96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
            20   25   30

CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG 144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
            35   40   45

GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG 192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
        50   55   60

TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG 240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65   70   75   80

GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA 288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
                85   90   95

CTC GAC AGG AAG GCG GCG GCG GCG GCG GGC GAG GCA GGG GCG TGG GGC 336
Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
            100   105   110

GGC GAT CGC GAG CCG CCA GCC GCG GGC CCA CGG GCG CTG GGG CCG CCC 384
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
            115   120   125

```
GCC GAG GAG CCG CTG CTC GCC GCC AAC GGG ACC GTG CCC TCT TGG CCC 432
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
    130                 135                 140

ACC GCC CCG GTG CCC AGC GCC GGC GAG CCC GGG GAG GAG GCG CCC TAT 480
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145                 150                 155                 160

CTG GTG AAG GTG CAC CAG GTG TGG GCG GTG AAA GCC GGG GGC TTG AAG 528
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
                165                 170                 175

AAG GAC TCG CTG CTC ACC GTG CGC CTG GGG ACC TGG GGC CAC CCC GCC 576
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
            180                 185                 190

TTC CCC TCC TGC GGG AGG CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC 624
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
            195                 200                 205

ATG GAG CCC GAC GCC AAC AGC ACC AGC CGC GCG CCG GCC GCC TTC CGA 672
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
    210                 215                 220

GCC TCT TTC CCC CCT CTG GAG ACG GGC CGG AAC CTC AAG AAG GAG GTC 720
Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225                 230                 235                 240

AGC CGG GTG CTG TGC AAG CGG TGC G                               745
Ser Arg Val Leu Cys Lys Arg Cys
                245
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 164:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 12
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys
  1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 5
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D)   OTHER INFORMATION: Xaa in position 1 is unknown.

165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Leu Val Leu Arg
 1   5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 11
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: Xaa in positions 1, 2, and 3 is
unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn
 1   5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 60
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in positions 25 and 36 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT   60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 18
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:

        (D) OTHER INFORMATION: N in position 16 is unknown.

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC   18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:

(i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 21
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```
Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
 1               5               10              15

Ile Gly Ala Tyr Thr
            20
```

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:

    (i) SEQUENCE CHARACTERISTICS:

    (A) LENGTH: 422
    (B) TYPE: amino acid
    (C) STRANDEDNESS:
    (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
 1               5               10              15

Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
            20              25              30

Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
            35              40              45

Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
    50              55              60

Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
 65              70              75              80

Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
                85              90              95

Leu Asp Arg Lys Ala Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
           100             105             110

Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
           115             120             125

Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
    130             135             140

Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145             150             155             160

Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
                165             170             175

Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
            180             185             190

Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
            195             200             205
```

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Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
    210   215   220

Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
225   230   235   240

Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu
            245   250   255

Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys
        260   265   270

Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn
        275   280   285

Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln
    290   295   300

Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
305   310   315   320

Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp
            325   330   335

Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr
        340   345   350

Ser Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys
        355   360   365

Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser
    370   375   380

Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp
385   390   395   400

Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
            405   410   415

Phe Leu Ser Leu Pro Glu
            420

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 69
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
  1   5   10   15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
            20   25   30

Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
        35   40   45

Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala

```
              50                    55                     60

Asn Thr Ser Ser Ser
 65


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     172:

    (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH:              19
         (B) TYPE:                amino acid
         (C) STRANDEDNESS:
         (D) TOPOLOGY:            linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1               5                   10                  15

Thr Thr Ala


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     173:

    (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH:              231
         (B) TYPE:                nucleic acid
         (C) STRANDEDNESS:        single
         (D) TOPOLOGY:            linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAGCGCC TCAGCGCGGC CGCTCGCTCT CCCCCTCGAG GGACAAACTT TTCCCAAACC 60

CGATCCGAGC CCTTGGACCA AACTGCCTG CGCCGAGAGC CGTCCGCGTA GAGCGCTCCG 120

TCTCCGGCGA GATGTCCGAG CGCAAAGAAG GCAGAGGCAA AGGGAAGGGC AAGAAGAAGG 180

AGCGAGGCTC CGGCAAGAAG CCGGAGTCCG CGGCGGGCAG CCAGAGCCCA G      231


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     174:

    (i) SEQUENCE CHARACTERISTICS:

         (A) LENGTH:              178
         (B) TYPE:                nucleic acid
         (C) STRANDEDNESS:        single
         (D) TOPOLOGY:            linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC CCGATTGAAA GAGATGAAAA GCCAGGAATC GGCTGCAGGT TCCAAACTAG 60

TCCTTCGGTG TGAAACCAGT TCTGAATACT CCTCTCTCAG ATTCAAGTGG TTCAAGAATG 120

GGAATGAATT GAATCGAAAA AACAAACCAC AAAATATCAA GATACAAAAA AAGCCAGG   178


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:     175:

    (i) SEQUENCE CHARACTERISTICS:
```

```
              (A) LENGTH:              122
              (B) TYPE:                nucleic acid
              (C) STRANDEDNESS:        single
              (D) TOPOLOGY:            linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA CTTCGCATTA ACAAAGCATC ACTGGCTGAT TCTGGAGAGT ATATGTGCAA 60

AGTGATCAGC AAATTAGGAA ATGACAGTGC CTCTGCCAAT ATCACCATCG TGGAATCAAA 120

CG                                                                   122


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    176:

     (i) SEQUENCE CHARACTERISTICS:

              (A) LENGTH:              102
              (B) TYPE:                nucleic acid
              (C) STRANDEDNESS:        single
              (D) TOPOLOGY:            linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC TGGTATGCCA GCCTCAACTG AAGGAGCATA TGTGTCTTCA GAGTCTCCCA 60


TTAGAATATC AGTATCCACA GAAGGAGCAA ATACTTCTTC AT                       102


(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    177:

     (i) SEQUENCE CHARACTERISTICS:

              (A) LENGTH:              128
              (B) TYPE:                nucleic acid
              (C) STRANDEDNESS:        single
              (D) TOPOLOGY:            linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAA ATGTGCGGAG AAGGAGAAAA 60

CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT 120

ACTTGTGC                                                             128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    178:

     (i) SEQUENCE CHARACTERISTICS:

              (A) LENGTH:              69
              (B) TYPE:                nucleic acid
              (C) STRANDEDNESS:        single
              (D) TOPOLOGY:            linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA 60

AACCAAGAA                                                            69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER:    179:
```

(i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 23
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA   23

    (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180:

            (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 23
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT   23

    (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181:

            (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 22
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCCTCCTT GA   22

    (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182:

            (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 22
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA   22

    (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183:

            (i) SEQUENCE CHARACTERISTICS:

                (A) LENGTH: 20
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 20
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GGCGGCGAAA   20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 185:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 15
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

Glu Gly Lys Val His Pro Gln Arg Arg Gly Ala Leu Asp Arg Lys
               5   10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 186:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 17
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu
               5   10   15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 187:

    (i) SEQUENCE CHARACTERISTICS:

        (A) LENGTH: 16
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln Lys Lys
               5   10   15

(2) INFORMATION FOR SEQ ID NO:188:

    (i) SEQUENCE CHARACTERISTICS:

```
        (A)  LENGTH: 151 amino acids
        (B)  TYPE: amino acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: peptide

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:188:

Cys Thr Ala Cys Ala Thr Cys Thr Ala Cys Ala Thr Cys Cys Ala Cys
 1               5                  10                  15
Cys Ala Cys Thr Gly Gly Gly Ala Cys Ala Ala Gly Cys Cys Ala Thr
            20                  25                  30
Cys Thr Thr Gly Thr Ala Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly
        35                  40                  45
Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Ala Ala Cys Thr Thr Thr
        50                  55                  60
Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly Gly
65                  70                  75                  80
Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala
                85                  90                  95
Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys Ala Ala Ala Cys Cys Cys
            100                 105                 110
Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys
            115                 120                 125
Thr Cys Gly Gly Gly Cys Thr Cys Cys Ala Thr Gly Ala Ala Gly Ala
    130                 135                 140
Ala Gly Ala Thr Gly Thr Ala
145                 150

(2) INFORMATION FOR SEQ ID NO:189:

        (i)  SEQUENCE CHARACTERISTICS:
        (A)  LENGTH: 211 amino acids
        (B)  TYPE: amino acid
        (C)  STRANDEDNESS: single
        (D)  TOPOLOGY: linear

    (ii)  MOLECULE TYPE: peptide

    (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:189:

Cys Thr Ala Cys Ala Thr Cys Thr Ala Cys Ala Thr Cys Cys Ala Cys
 1               5                  10                  15
Cys Ala Cys Thr Gly Gly Gly Ala Cys Ala Ala Gly Cys Cys Ala Thr
            20                  25                  30
Cys Thr Thr Gly Thr Ala Ala Ala Ala Thr Gly Thr Gly Cys Gly Gly
        35                  40                  45
Ala Gly Ala Ala Gly Gly Ala Gly Ala Ala Ala Ala Cys Thr Thr Thr
        50                  55                  60
Cys Thr Gly Thr Gly Thr Gly Ala Ala Thr Gly Gly Ala Gly Gly Gly
65                  70                  75                  80
Gly Ala Gly Thr Gly Cys Thr Thr Cys Ala Thr Gly Gly Thr Gly Ala
                85                  90                  95
Ala Ala Gly Ala Cys Cys Thr Thr Thr Cys Ala Ala Ala Cys Cys Cys
            100                 105                 110
Cys Thr Cys Gly Ala Gly Ala Thr Ala Cys Thr Thr Gly Thr Gly Cys
            115                 120                 125
Ala Ala Gly Thr Gly Cys Cys Ala Ala Ala Thr Gly Ala Ala Gly Thr
    130                 135                 140
Thr Thr Ala Cys Thr Gly Gly Thr Gly Ala Thr Cys Gly Cys Thr Gly
145                 150                 155                 160
Cys Cys Ala Ala Ala Ala Cys Thr Ala Cys Gly Thr Ala Ala Thr Gly
            165                 170                 175
Gly Cys Cys Ala Gly Cys Thr Thr Cys Thr Ala Cys Thr Cys Cys Ala
```

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```
          180                 185              190
Thr Gly Ala Ala Gly Ala Ala Gly Ala Thr Gly Thr Ala Cys Cys Thr
          195                 200              205
Gly Cys Thr
          210
```

B' could

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